similarity, i.e. 20% or higher. The overall secondary structure consists almost entirely of pleated sheets and is low in α-helices. Each domain contains an active site centred on a catalytic aspartyl residue with a consensus sequence [hydrophobic]-Asp-Thr-Gly-[Ser/Thr] (SEQ ID NO:7) which aids in maintaining the correct Φ-loop conformation of the site, and with multiple hydrophobic residues near the aspartic residue. The two catalytic sites are arranged face-to-face in the tertiary structure of correctly folded proteins. In bovine chymosin, the distance between the aspartic side chains is about 3.5 Å. The residues are reported to be extensively hydrogen bonded, concomitantly with the adjacent threonine residues, to the corresponding residues of the other domain or the neighbouring atoms of the own domain, to stabilise the correct position. Optimum activity of an aspartic protease is achieved when one of the aspartic residues is protonated and the other one is negatively charged. The active sites of chymosin and other aspartic proteases are embedded, with low accessibility, in the middle of a cleft, about 40 Å in length, which separates the two domains, and which is covered by a flap that, in bovine and camel chymosin, extends from about Leu73 to Ile85 in the N-terminal domain.--